



SEQUENCE LISTING

<110> Scheirlein, Friedrich
Kerschbaumer, Randolph
Falkner, Falko-Guenter
Dorner, Friedrich

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<140> US 09/661,992

<160> 176

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 1

ctcaatttttc ttgtccacct tgggtgc

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<210> 2

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<221> Description of the artificial sequence:primer

<400> 2

ctcaatttttc ttgtatcaact cagtct

26

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<213> Artificial Sequence

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<221> Description of the artificial sequence:primer

<400> 3

tggatatgggc acatgcagat ctct

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<210> 4

<211> 24

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<220>

<221> Description of the artificial sequence:primer

<400> 4

ctcaattcctg ttgaagctct tgac

24

<210> 5
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<220>
<221> Description of the artificial sequence:CDR3 region

<430> 5
Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr
1 5 10

<210> 6
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<213> Artificial Sequence

<220>
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<430> 6
Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr
5 10

<210> 7
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<220>
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<430> 7
Asp Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 8
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<430>
Asp Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val
5 10

<210> 9
<211> 13
<212> PRT
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<220>
<221> Description of the artificial sequence:CDR3 region

<430> 9

Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 13
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<212> PRT
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:CDR3 region

<400> 10
Val Tyr Gly Phe Gly Trp Gly Tyr Glu Val Asn Asp Tyr
1 5 10

<210> 11
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 11
Glu Glu Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Glu
1 5 10 15

Glu Glu

<210> 11
<211> 18
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<220>
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<400> 12
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 13
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:CDR3 region

<400> 13
Glu Tyr Gly Glu Gly Tyr Gly Glu Val Asn Glu Tyr Asp Glu Phe Glu
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Trp Glu

<210> 14
<211> 16
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<220>
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<400> 14
Val Arg Tyr Arg Asn Arg Tyr Arg Trp Gly Tyr Arg Gly Arg Phe Gly
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Asp Glu

<210> 15
<211> 18
<212> PRT
<213> Artificial Sequence

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<400> 15
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg
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Arg Arg

<210> 16
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<220>
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<400> 16
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
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Arg Arg

<210> 17
<211> 18
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<400> 17
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg
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Arg Arg

<210> 16
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<213> Artificial Sequence

<220>
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<400> 16
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15
Arg Arg

<210> 19
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 19
Arg Arg Arg Ala Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
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Arg Arg

<210> 20
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<212> PRT
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<220>
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<400> 20
Arg Arg Arg Glu Ala Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
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Arg Arg

<210> 21
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<220>
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<400> 21
Arg Arg Arg Glu Gly Ala Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 22
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 22
Arg Arg Arg Glu Gly Gly Ala Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<110> 23
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<120>
<123> Description of the artificial sequence:CDR3 region

<400> 23
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Arg Arg

<210> 24
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 24
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1 5 10 15

Arg Arg

<210> 25
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 25
Arg Arg Arg Glu Gly Gly Tyr Tyr Ala Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 26
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 26
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Ala Trp Tyr Phe Asp Arg
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Arg Arg

<210> 27
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 27
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Ala Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 28
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 28
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Ala Phe Asp Arg
1 5 10 15

Arg Arg

<210> 29
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 29
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Ala Asp Arg

1

5

10

15

Arg Arg

<210> 30
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 30
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Ala Arg
1 5 10 15

Arg Arg

<210> 31
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 31
Arg Arg Arg Tyr Val Tyr Asn Gly Trp Gly Tyr Phe Glu Gly Ala Arg
1 5 10 15

Arg Arg

<210> 32
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 32
Arg Arg Arg Glu Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 33
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 33

A: Arg Arg Glu Gly Glu Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
5 10 15

A: Arg

<_10> 34
<_11> 18
<_12> PRT
<_13> Artificial Sequence

<_10>
<_13> Description of the artificial sequence:CDR3 region

<_10> 34
A: Arg Arg Glu Gly Glu Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

A: Arg

<_10> 35
<_11> 18
<_12> PRT
<_13> Artificial Sequence

<_10>
<_13> Description of the artificial sequence:CDR3 region

<_10> 35
Arg Arg Arg Glu Gly Glu Gly Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<_10> 36
<_11> 18
<_12> PRT
<_13> Artificial Sequence

<_10>
<_13> Description of the artificial sequence:CDR3 region

<_10> 36
Arg Arg Arg Glu Gly Glu Gly Tyr Glu Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<_10> 37
<_11> 18
<_12> PRT
<_13> Artificial Sequence

<_10>
<_13> Description of the artificial sequence:CDR3 region

<400> 37

Arg Arg Arg Glu Gly Gly Tyr Tyr Glu Asn Trp Tyr Phe Asp Arg
1 5 10 15

A: β Arg

<310> 38

<311> 18

<312> PRT

<313> Artificial Sequence

<320>

<323> Description of the artificial sequence:CDR3 region

<400> 38

A: β Arg Arg Glu Gly Gly Tyr Tyr Val Glu Trp Tyr Phe Asp Arg
1 5 10 15

A: β Arg

<110> 39

<111> 18

<112> PRT

<113> Artificial Sequence

<120>

<123> Description of the artificial sequence:CDR3 region

<400> 39

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Glu Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<110> 40

<111> 18

<112> PRT

<113> Artificial Sequence

<120>

<123> Description of the artificial sequence:CDR3 region

<400> 40

Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Glu Phe Asp Arg
1 5 10 15

Arg Arg

<110> 41

<111> 18

<112> PRT

<113> Artificial Sequence

<120>

<123> Description of the artificial sequence:CDR3 region

<400> 41
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Glu Asp Arg
1 5 10 15

Arg Arg

<210> 42
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 42
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Glu Arg
1 5 10 15

Arg Arg

<210> 43
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 43
Arg Arg Arg Gly Glu Tyr Gly Glu Tyr Trp Asn Gly Asp Phe Tyr Arg
1 5 10 15

Arg Arg

<210> 44
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 44
Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 45
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 45

Arg Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
1 5 10

<210> 46
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 46
Phe Gly Val Gly Tyr Arg Gly Glu Thr Arg Asn Phe Asp Trp
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<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 47
Glu Glu Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Glu
1 5 10 15

Glu Glu

<210> 48
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 48
Arg Arg Arg Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 49
<211> 18
<212> PFT
<213> Artificial Sequence

<220>
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<400> 49
Arg Arg Arg Phe Gly Val Gly Tyr Gly Glu Thr Asn Phe Asp Trp Arg
1 5 10 15

Arg Arg

<210> 50
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

<400> 50
gtatgcatga ctgcggccat agccggccat ggccsaggtt marctgcags agtcawgg 57

<210> 51
<211> 56
<212> DNA
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<220>
<223> Description of the artificial sequence:primer

<400> 51
gtatctcgaa ctgcggccaa gcggccatg gccgaggtgc agcttcagga gtcagg 58

<210> 52
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:primer

<400> 52
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<210> 53
<211> 56
<212> DNA
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<220>
<223> Description of the artificial sequence:primer

<400> 53
gtatctcgaa ctgcggccaa gcggccatg gcccaggtgc agctgaagsa gtcagg 59

<210> 54
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<220>
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<400> 54
gtatctcgaa ctgcggccaa gcggccatg gccgaggttc agctgcarca rtctgg 56

<210> 55

<211> 56
<212> DNA
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<22>
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gtatcggaa ctgcggccca gcccggccatg gcccagggttc aatgtggatc gtttgg
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<21> 56
<211> 56
<212> DNA
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<22>
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<40> 56
gtatcggaa ctgcggccca gcccggccatg gcccggccatg agctgggttga rtctgg
56

<21> 57
<211> 56
<212> DNA
<213> Artificial Sequence

<22>
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<40> 57
gtatcggaa ctgcggccca gcccggccatg gcccggccatg agctttagca gtctgg
56

<21> 58
<211> 56
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<22>
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<40> 58
gtatcggaa ctgcggccca gcccggccatg gcccggccatg agctggatgc agctgktgg
56

<21> 59
<211> 56
<212> DNA
<213> Artificial Sequence

<22>
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<40> 59
gtatcggaa ctgcggccca gcccggccatg gcccggccatg agctggatgc agctgktgg
56

<21> 60
<211> 68
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

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atccgtcagat ggcgcgcac ctgaaccgc tccacctgag gagacggtga ccgtggtccc 60
tttggccccc

<210> 61

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<400> 61

atccgtcagat ggcgcgcac ctgaaccgc tccacctgag gagacggtga ccgtggtccc 60

<210> 62

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<400> 61

atccgtcagat ggcgcgcac ctgaaccgc tccacctgag gagacgtgtga gagtggtgcc 60

<210> 63

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<400> 63

atccgtcagat ggcgcgcac ctgaaccgc tccacctgca gagacagtga ccagagtccc 60

<210> 64

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

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atccgtcagat ggcgcgcac ctgaaccgc tccacctgag gagacggtga ctgaggttcc 60

<210> 65

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<10> 65

gtttcagatg ggccggcctc tggcggtggc ggatcggaca ttgtgttac acgtctcc 65

<11> 66

<111> 59

<112> DNA

<113> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<10> 66

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<11> 67

<111> 59

<112> DNA

<113> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<10> 67

gtttcagatg ggccggcctc tggcggtggc ggatcggatg ttktgtatgac ccaaactcc 67

<11> 68

<111> 59

<112> DNA

<113> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<10> 68

gtttcagatg ggccggcctc tggcggtggc ggatcggata ttgtgtatrac bcaggcwg 68

<11> 69

<111> 59

<112> DNA

<113> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<10> 69

gtttcagatg ggccggcctc tggcggtggc ggatcggaca ttgtgtatqac mcartctcc 69

<11> 70

<111> 59

<112> DNA

<113> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<10> 70

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<210> 71
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<230> Description of the artificial sequence:primer

<400> 71
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<210> 72
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
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<400> 72
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<210> 73
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<230> Description of the artificial sequence:primer

<400> 73
ggttcagatg ggccgcgcctc tggccgtggc ggatccgtcat tattgcagggt gcttgtggg 59

<210> 74
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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<400> 74
gttttattctt gggccgcctc gtttgcatttc cagcttggtg cc 42

<210> 75
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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<400> 75
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<21> 76
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<21> DNA
<21> Artificial Sequence

<22>
<22> Description of the artificial sequence:primer

<40> 76
gttttattctt gggggcgccc gttttatttc cagttggtc cc 42

<21> 77
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<21> DNA
<21> Artificial Sequence

<22>
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<40> 77
gttttattctt gggggcgccc gttttatttc caactttgtc cc 42

<21> 78
<21> 42
<21> DNA
<21> Artificial Sequence

<22>
<22> Description of the artificial sequence:primer

<40> 78
gatcattttt gggggcgccc gtttcagctc cagttggtc cc 42

<21> 79
<21> 74
<21> DNA
<21> Artificial Sequence

<22>
<22> Description of the artificial sequence:mychis 6

<40> 79
ggggccagaa caaaaactca tctcagaaga ggatctgaat gggggggcac atcaccatca 60
caatcaactaa taag 74

<21> 80
<21> 74
<21> DNA
<21> Artificial Sequence

<22>
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<40> 80
attttttattt agtgatggtg atggtgatgt gcccggccat tcagatcctc ttctgagatg 60
attttttgtt ctgc 74

<21> 81

<211> 726
<212> DNA
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4123 Description of the artificial sequence:scFv region

4460	61					
tgagg-gaaggc	tggtggagtc	tggacctgag	ctgaagaaga	cggagagac	agtcaagatc	61
tatcttcagg	ctctgggta	tatcttcaca	aactatggaa	ttaactgggt	aaagcaggct	120
ccAGuaaaagg	ttttaaagtgc	gatgggtctgg	ataaaacacct	awactggaga	cccaacatata	180
gttgtgtact	tcaagggacg	gtttgcttcc	tctttggaaa	cctctgcacg	cactgcctat	240
ttttcAgatca	acaacccaa	aatatgaggac	acggctacat	atttttgtgc	attatatgtt	300
aaatttcccta	aggggtttgc	ttactggggs	caagggactc	ttgttcaatgt	ctctgcagg	360
ggaggccgtt	cagtggggcg	cgctctggc	ggtggggat	ccggatattca	gatgacacacg	420
tcttcggaaat	tcctgttgt	atcaggcagg	gacagggita	ccataacccg	caaggccagt	480
ccagatgtga	gtaatqatgt	agtttggac	caacagaags	ccggggcagc	tcctaaaacta	540
cttcatgtact	atgcattcaa	tcgttacact	ggagtccctg	atcgcttcac	tggcagtgga	600
ttatggacgg	atttcacttt	caccatcagg	actgtgcagg	ctgaagacat	ggcagtttat	660
tttttttcagg	agjattatgg	ctcttcctcc	asgttccggag	ggggccacaa	gttggaaatt	720
aaaaacgg						726

<210 82
<211 242
<212 PRT
<213 Artificial Sequence

<2.20>
<2.23> Description of the artificial sequence: scFv region

410-82
Glu Val Lys Leu Val Glu Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr
 20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
56 55 50

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80

Leu Ser Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95

Ala Leu Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Arg Ala
115 120 125

Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Lys Phe
 130 135 140

Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser
 145 150 155 160

Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln

Ser Pro Lys Ileu Ileu Met Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val
 180 185 190

Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr
 135 200 205

Leu Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
214 215 216 217 218 219 220

Asp Tyr Gly Ser Pro Pro Thr Ile Gly Gly Gly Thr Lys Ile Glu Ile
 230 231 232 233 234 235 236 237 238 239 240 241

lys ring

<110> 83
<111> T47
<112> DNA
<113> Artificial Sequence

• 20 •

4.2.3) Description of the artificial sequence: scFv region

10. 84
11. 249
12. PRT
13. Artificial Sequence

Q23. Description of the artificial sequence:scFv region

84
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
 50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Thr Arg Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly Gly
 115 120 125
 Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro
 130 135 140
 Ile Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 145 150 155 160
 Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp
 165 170 175
 Tyr Ile Gln Lys Pro Gly Gln Ser Pro Lys Leu Ile Ile Tyr Lys Val
 180 185 190
 Ser Asn Arg Phe Ser Gly Val Pro Asp Lys Phe Ser Gly Ser Gly Ser
 195 200 205
 Gly Thr Asp Phe Thr Ile Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 210 215 220
 Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly
 225 230 235 240
 Gly Gly Thr Lys Leu Glu Ile Lys Arg
 245

110: 85
111: "47
112: DNA
113 Artificial Sequence

120
123. Description of the artificial sequence: scFv region.

```

:000 85
gttgtcagc ttcaaggagtc agggggagjc ttagtgaagc ctgjagggtc octgaaaactc 60
tttttgtcag cttctggatt cactttcajt agctatacca tggttttgggt tggcccajact 100
ccggagaaga ggcttggagtg gtttgtcaacc atttagtagtg jggggagttc cacstataat 140
ccagacatgt tjaaggccj attccatcc tccagagaca atggccaaagaa cacccttjtac 240
ctgtcaatgtg gcaagctgag gtctgaggac acagccatgt attatgtgtac aagjagaaagggg 300
gggttgttca csgtcaactg gtacttcgat gtctggggcg cagggactct jgtcacttgtc 360
tttgtggaggtg gaggggggttc aagggtggcg gcttctggcg jgggggggatc jgaaaatgtg 420
cttacccatgt ctccagcttc ttgtgtgtg tctcttagggc agaggjggccac tataatctgc 480
agaggccatgt aaagtgttga tagttatggc tataattttt tgcacttgta tcagcagata 540
ccaggacacgc cacccaaact cttcatstat cgtgcattca acctagatgc tgggatccct 600
ccctggatgtca gtggcaatgg gctctaggaca gacttcaccc taccattaa tctgtggag 660
gttgtatgttgc aactgttca ttactgtcag caaagtaatg aggtatccjct caccgttgggt 720
actgggacca gactggaaat aaaaacgg 747

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<210> 86
<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 86

Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Tyr Arg Glu Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp
100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Ser Gly
115 120 125

Gly Arg Ala Ser Gly Gly Ser Gly Ser Glu Asn Val Leu Thr Gln Ser
130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
145 150 155 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp
165 170 175

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
180 185 190

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
225 230 235 240

Thr Gly Thr Arg Leu Glu Ile Lys Arg
245

<210> 87

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

400> f7
gttgtccaaac ttcaaggagtc agggggagtc ttatgtaaac ctggadggc cctgaaaactc 4
ttttgtgtcg cctctggatt catttttagt agttataacca tggcttgggt tggccagast 11
ccggagaaga ggttggagtg ggtccaaacc attatgtgt gtggtagtc caactactat 11
ccatggacatgt tgaaaggcccg attccaccatc tccagagaca atgccaajaa caccctgtac 24
atgtcaatgtt gcaatctgtaa gtgtgaggac acagccatgt atcaactgtac aagagagggg 13
ttttttttttt acitcaactg gtatccatgt gtcttgggggg cagccacccac tctccatgtc 16
ttttcaatgtt caatgggttc agttggggccg gctcttgggg gtggggatc ggacatttgay 41
atcaacnagt ctccatgttc tttaggggtt ttcctadggc agagggccac cattatctgt 41
agagccatgtt aaagtgttga tagttatggc aagagttttt tgcactggta ccagcagaaa 14
ccagggccatc cacccaaact cttcatctat cgtgcattcc acatagaatc tgggatccct 63
ccatgggttc gttttttttt gttttttttt gttttttttt tttttttttt tttttttttt 63
gtttttttttt ttgtttttttt ttatgtttttt tttttttttt tttttttttt tttttttttt 63
gtttttttttt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 63
gtttttttttt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 63

(210) 58

4211 243

212 FRT

213 Artificial Sequence

220:

223> Description of the artificial sequence: scFv region

400: 88

Glu Val Gln Leu Gln Ser Gly Gly Gly Leu Val Lys Pro Phe Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 71 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys
85 90 95

Thr Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val Trp
 100 105 110

Gly Ala Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125

Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser
 130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
 148 151 154 155 156 157 158 159 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His Trp
 165 170 175

Tyr Gin Gln Lys Pro Gly Gin Pro Pro Lys Leu Leu Ile Tyr Arg Ala
 180 181 182 183 184 185 186 187 188 189 190 191 192 193

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser

144

23

20 cm

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
 210 215 220
 Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
 225 230 235 240
 Ala Gly Thr Arg Leu Glu Ile Lys Arg
 245

<210> 19
<211> DNA
<212> DNA
<213> Artificial Sequence

<220> <223> Description of the artificial sequence:scFv region

<210> 90

<211> 732

<212> FFT

<213> Artificial Sequence

<221>

<222> Description of the artificial sequence: scFv region

<223> 16

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Glu Ile Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn
115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
130 135 140

Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Asp
145 150 155 160

Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
225 230 235 240

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
260 265 270

Ala Ala Ala Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala
275 280 285

Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp
290 295 300

Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn
305 310 315 320

Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala
325 330 335

Ala Arg Asn Tyr Ala Glu Gly Ala Gly Phe Phe Lys Gly Ile Asp
340 345 350

Ala Leu Pro Leu Thr Gly Gin Tyr Thr His Tyr Ala Leu Asn Lys Lys
355 360 365

Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala
370 375 380

Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile
385 390 395 400

His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly
405 410 415

Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gin Asp Ala Thr Pro
420 425 430

Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser
435 440 445

Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Lys
450 455 460

Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu
465 470 475 480

Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp
485 490 495

Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu
500 505 510

Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln
515 520 525

Lys Pro Leu Leu Gly Ile Phe Ala Asp Gly Asn Met Pro Val Arg Trp
530 535 540

Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val
545 550 555 560

Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala
565 570 575

Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly
580 585 590

Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala
595 600 605

Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala
610 615 620

Val Gln Arg Ala Leu Glu Phe Ala Lys Glu Gly Asn Thr Leu Val
625 630 635 640

Thr Lys Ala Pro Gly Ileu Thr Glu Ala Ileu Asn Thr Lys Asp Glu Ala
661 662 663 664 665 666 667 668 669 670 671 672 673

Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His
 675 680 685

Thr Gly Ser Gin Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn
690 695 700

Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala
705 710 715 720

Ala Leu Gly Asp Ile Ala His His His His His His His
725 730

<210> P1
<211> 973
<212> DNA
<213> Artificial Sequence

<1120> <1137> Description of the artificial sequence: scFv region

<211> 32
<2111> 325
<2112> PRT
<2113> Artificial Sequence

123 Description of the artificial sequence: scFv region

4000-92
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Ser Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

35

40

45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
 50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
 65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
 100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Phe Thr Val Asn
 115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
 130 135 140

Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Ser Asp
 145 150 155 160

Ile Val Leu Thr Gln Xaa Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
 165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
 180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
 195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
 210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
 225 230 235 240

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
 245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
 260 265 270

Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln
 275 280 285

Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu
 290 295 300

Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His
 315 310 320

His His His His His
 325

<10> 93

<11> 2190

<12> DNA

<13> Artificial Sequence

<20>

4.23. Description of the artificial sequence: scFv region

卷之三

100

<11> 723

卷之三

113 Artificial Sequence

322

<12> Description of the artificial sequence: siIV region

<40.0> 94

Met Lys Tyr Leu Ile Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gin Gin Ser Gly Pro Glu
 20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
50 55 60

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
65 70 75 80

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
100 105 110

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
130 135 140

Gly Ser Gly Gly Arg Ala Ser Gly Gly Ser Gln Ile Val Leu
145 150 155 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
165 170 175

Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
180 185 190

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
195 200 205

Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
225 230 235 240

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
245 250 255

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala
260 265 270

Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp
275 280 285

Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala
290 295 300

Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu
305 310 315 320

Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn
325 330 335

Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro
340 345 350

Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys
355 360 365

Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr
370 375 380

Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys
385 390 395 400

Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr
405 410 415
Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu
420 425 430
Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser
435 440 445
Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile
450 455 460
Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly
465 470 475 480
Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys
485 490 495
Thr Leu Arg Glu Gln Ala Gin Ala Arg Gly Tyr Gln Leu Val Ser Asp
500 505 510
Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu
515 520 525
Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro
530 535 540
Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr
545 550 555 560
Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr
565 570 575
Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Ile
580 585 590
Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro
595 600 605
Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg
610 615 620
Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr
625 630 635 640
Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala
645 650 655
Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val
660 665 670
Met Ser Tyr Gly Asn Ser Gln Glu Asp Ser Gln Glu His Thr Gly Ser
675 680 685
Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly
690 695 700
Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly
705 710 715 720
Asp Ile Ala His His His His His
725

<210> 95
<211> 969
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:scFv region

<400> 96
atgaaaatacc tattgcctac ggcaagccgct ggatgtttat tactcgccgc ccagccggcc 60
atggccggagg ttccagctca gcaatctgtca cctgagctgg tgaagcccccgg ggcctcaatgt 120
aagattttctt gcaaaatgttc tggctacgca ttccatgtatctt ctggatgaa ctgggtgaag 160
cagaggccgtg gacagggtst tggatggatt ggacggatatt atctggaaa tggagatata 240
aactacaatg gggatgttcaa gggcaaggcc acaatgtactg cagacaaatcc ctccaggcaca 300
ccatcacatgc agtctccatgc ctttgcacatgt gtggatctgt cggctctatcc ttgtgcagat 360
ggtaacgtat attactatgc tatggactac tggggccaaag gaaaccttgcgttccatgttcc 420
tcagggtggag ggggttccagg tggggccggcc ttggggccgtg gggatgtcga aattgttcc 480
acccatgttc ctgtttccat agtctgtatctt ctggggccaga gggccatccatgttccatgttcc 540
gcacacaaatggatgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttcc 600
ngacacggccatccatgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttcc 660
nggttccatgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttcc 720
naggatgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttcc 760
ngcacacaaatggatgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttcc 840
*cccatatgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttcc 900
caaaacgggg tagctgttccatgttccatgttccatgttccatgttccatgttccatgttccatgttcc 960
caccattaa 969

<210> 96
<211> 322
<212> PRT
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:scFv region

<400> 96
Met Lys Tyr Leu Ieu Pro Thr Ala Ala Ala Gly Leu Ieu Leu Leu Ala
1 5 10 15
Ala Glu Phe Ala Met Ala Glu Val Gln Leu Gln Ser Gly Pro Glu
20 25 30
Leu Val Lys Phe Gly Ala Ser Val Lys Ile Ser Cys Iys Ala Ser Gly
35 40 45
Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
50 55 60
Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
65 70 75 80
Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
85 90 95
Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
100 105 110
Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
115 120 125
Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly

130	135	140	
Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly	Ser Gln Ile Val Leu		
145	150	160	
Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr			
165	170	175	
Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr			
180	185	190	
Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile			
195	200	205	
Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly			
210	215	220	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu			
225	230	240	
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg			
245	250	255	
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Pro			
260	265	270	
Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln Leu Glu Asp			
275	280	285	
Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val			
290	295	300	
Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His His His His			
305	310	315	320
His His			

<210> 97
 <211> 270
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the artificial sequence:scFv region

<400> 97
 caggaaacag ctatgaccat gattacgcga agcttccatg aaaattctat ttcaaggaga 60
 cagtccataat gaaataccctt ttgtccatccgg cagccgcgtgg attgtttatta ctcgcgggccc 120
 agccggccat ggcccgagggtg caggtgcagg cgcgcctgcga ggtcgacccctc gagatccaaac 180
 ggcgcgcgc agaacaaaaaa ctcatctcaag aagaggatct gaatggggcg gcacatccacc 240
 atcaccatca ctaataagaa ttactggcc 270

<210> 98
 <211> 61
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of the artificial sequence:scFv region

400> P6
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 10 19 28 37 46 55 64 73 82 91 100
 Ala Glu Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu Gln Val
 10 20 30 40 50 60 70 80 90 100
 Asp Leu Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser Glu
 10 20 30 40 50 60 70 80 90 100
 Glu Asp Leu Asn Gly Ala Ala His His His His His His His His
 50 60 70 80 90 100

<210> 39
<211> 866
<212> DNA
<213> Artificial Sequence

and description of the artificial sequence:scFv region

<2100> 100
<2110> 294
<2120> PRT
<2130> Artificial Sequence

1.230 Description of the artificial sequence:scfV region

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Aaa Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
 20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
51 55 60 62

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
 65 70 75 80

- 210 - 101

S. 2112 875

1122 2023

213 Artificial Sequence

<220>

<223> Des

ggacagccac cc当地actctt catcttatctt gcatccaaac tagaatctgg ggtccctggc
gggttcgttg gcagttgggtc tgggacacac ttccacccctca acatccatcc tggggadggg
ggatgttg cacccttatta ctctccaccac ayttagggagc ttctctggac gttcggttgg
ggccaccaac tggaaaatcaa acgggggggtc gcaaggacaaaa aictctatctc adaagaggat
gtggatctttt ccacacatca ccattaccat cacttta

2100 102
2111 201
2112 202
2113 Artificial Sequence

<220>
<223> Description of the artificial sequence:scFv region

<400> 102
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
23 24 25 26 27 28 29 30

Ile Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly

Gln Gly Leu Gln Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
102 103 104 105 106 107 108 109 110

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Tyr Ala Met
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Ser Gln Ile Val Leu
 145 150 155 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
 165 170 175

Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 180 185 190

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 195 200 205

Tyr Ile Ala Ser Asn Ile Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
225 230 235 240

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
245 250 255

Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu
260 265 270

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His
275 280 285

His His His
290

<210> 103

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 103

ggccgcagaa caaaaactca ttcagaaga ggatctgaat gggcggcac atcaccatca 60
ccatcaactaa taag 74

<210> 104

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:primer

<400> 104

ttattatgtt tggatgtt gatgtqccgc cccatccaga tcctttctg agatgagtt 60
tgttgttgc 69

<210> 105

<211> 16

<212> FRT

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:CDR3 region

<400> 105

Cys Xaa Xaa Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Xaa Xaa Cys
1 5 10 15

<210> 106

<211> 16

<212> FRT

<213> Artificial Sequence

<220>

<221> Description of the artificial sequence:CDR3 region

<400> 106

Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asx
1 5 10 15